SEQUENCE LISTING

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<120> NEW SYSTEMS FOR THE REGULATION OF GENE EXPRESSION

<130> 564-9005

<140> 09/147,693
<141> 1999-02-17

<150> PCT/EP97/04560
<151> 1997-08-21

<150> DE/196 33 698.8
<151> 1996-08-21

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<170> PatentIn Ver. 2.0

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<213> Lambda-OR-Operator (wild type)

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ctctggcggt gataatggtt gc 82

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<213> Lambda-OR-Operator (mutant)

a1

<400> 2
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ctctggcggt gataatggtt gc 82

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aggccactga ctagcgataa ctttccccac aacggaacaa ctctcattgc atgggatcat 180

tgggtactgt gggtttagtg gttgtaaaaa cacctgaccg ctatccctga tcagtttctt 240

gaaggtaaac tcatcacccc caagtctggc tatgcagaaa tcacctggct caacagcctg 300

ctcagggtca acgagaatta acattccgtc aggaaagctt ggcttggagc ctgttggtgc 360

ggtcatggaa ttaccttcaa cctcaagcca gaatgcagaa tcactggctt ttttggttgt 420

gcttacccat ctctccgcat caccttttggt aaaggttcta agcttaggtg agaacatccc 480

tgcctgaaca tgagaaaaaa cagggtactc atactcactt ctaagtgacg gctgcatact 540

aaccgcttca tacatctcgt agatttctct ggcgattgaa gggctaaatt cttcaacgct 600

aactttgaga atttttgtaa gcaatgcggc gttataagca tttaatgcat tgatgccatt 660

aaataaagca ccaacgcctg actgccccat ccccatcttg tctgcgacag attcctggga 720

taagccaagt tcatttttct ttttttcata aattgcttta aggcgacgtg cgtcctcaag 780

ctgctcttgt gttaatggtt tctttttttgt gctcatacgt taaatctatc accgcaaggg 840

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gtactaagta ggttgtatgg aacaacgcat aaccctgaaa gattatgcaa tgcgctttgg 960

gcaaaccaag acagctaaag atcctctaga gtcgacctgc aggcatgcaa gcttatcgaa 1020

ttctcattca ggcttctgcc gttttggatt taaccgaaga tgatttcgat tttctgacga 1080

gtaacaaagt ttggattgct actgaccgct ctcgtgctcg tcgctgcgtt gaggcttgcg 1140

ttt atg gta cgc tgg act ttg tgg gat acc ctc gct ttc ctg ctc ctg 1188
Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu Leu Leu
1 5 10 15

ttg agt tta ttg ctg ccg tca ttg ctt att atg ttc atc ccg tca aca 1236
Leu Ser Leu Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro Ser Thr
20 25 30

ttc aaa cgg cct gtc tca tca tgg aag gcg ctg aat tta cgg aaa aca 1284

```
Phe Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr
            35                  40                  45

tta tta atg gcg tcg agc gtc cgg tta aag ccg ctg aat tgt tcg cgt  1332
Leu Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg
         50                  55                  60

tta cct tgc gtg tac gcg cag gaa aca ctg acg ttc tta ctg acg cag  1380
Leu Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln
     65                  70                  75

aag aaa acg tgc gtc aaa aat tac gtg cag aag gag tgatgtaatg       1426
Lys Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
 80                  85                  90

tctaaaggta aaaaacgttc tggcgctcgc cctggtcgtc cgcagccgtt gcgaggtact 1486

aaaggcaagc gtaaaggcgc tcgtctttgg tatgtaggtg gtcaacaatt ttaattgcag 1546

gggcttcggc ccttacttga ggataaatta tgtctaatat tcaaactggc gccga      1601


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<212> PRT
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  1               5                  10                  15

Arg Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu
            20                  25                  30

Ser Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val
         35                  40                  45

Gly Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala
     50                  55                  60

Leu Leu Thr Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser
 65                  70                  75                  80

Ile Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Gln Pro
                85                  90                  95

Ser Leu Arg Ser Glu Tyr Glu Tyr Pro Val Phe Ser His Val Gln Ala
            100                 105                 110

Gly Met Phe Ser Pro Lys Leu Arg Thr Phe Thr Lys Gly Asp Ala Glu
        115                 120                 125

Arg Trp Val Ser Thr Thr Lys Lys Ala Ser Asp Ser Ala Phe Trp Leu
    130                 135                 140

Glu Val Glu Gly Asn Ser Met Thr Ala Pro Thr Gly Ser Lys Pro Ser
145                 150                 155                 160

Phe Pro Asp Gly Met Leu Ile Leu Val Asp Pro Glu Gln Ala Val Glu
```

a' cont

```
                165                 170                 175

Pro Gly Asp Phe Cys Ile Ala Arg Leu Gly Gly Asp Glu Phe Thr Phe
            180                 185                 190

Lys Lys Leu Ile Arg Asp Ser Gly Gln Val Phe Leu Gln Pro Leu Asn
        195                 200                 205

Pro Gln Tyr Pro Met Ile Pro Cys Asn Glu Ser Cys Ser Val Val Gly
    210                 215                 220

Lys Val Ile Ala Ser Gln Trp Pro Glu Glu Thr Phe Gly
225                 230                 235


<210> 6
<211> 91
<212> PRT
<213> pAW12 Fragment

<400> 6
Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu Leu Leu Leu
  1               5                  10                  15

Ser Leu Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro Ser Thr Phe
            20                  25                  30

Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr Leu
        35                  40                  45

Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg Leu
    50                  55                  60

Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln Lys
65                  70                  75                  80

Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
                85                  90


<210> 7
<211> 2834
<212> DNA
<213> pCSJ Fragment

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<222> (1025)..(2104)

<220>
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<222> (2377)..(2649)

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a' cont.

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aggccactga ctagcgataa ctttccccac aacggaacaa ctctcattgc atgggatcat 180

tgggtactgt gggtttagtg gttgtaaaaa cacctgaccg ctatccctga tcagtttctt 240

gaaggtaaac tcatcacccc caagtctggc tatgcagaaa tcacctggct caacagcctg 300

ctcagggtca acgagaatta acattccgtc aggaaagctt ggcttggagc ctgttggtgc 360

ggtcatggaa ttaccttcaa cctcaagcca gaatgcagaa tcactggctt ttttggttgt 420

gcttacccat ctctccgcat caccttttggt aaaggttcta agcttaggtg agaacatccc 480

tgcctgaaca tgagaaaaaa cagggtactc atactcactt ctaagtgacg gctgcatact 540

aaccgcttca tacatctcgt agatttctct ggcgattgaa gggctaaatt cttcaacgct 600

aactttgaga atttttgtaa gcaatgcggc gttataagca tttaatgcat tgatgccatt 660

aaataaagca ccaacgcctg actgccccat ccccatcttg tctgcgacag attcctggga 720

taagccaagt tcatttttct ttttttcata aattgcttta aggcgacgtg cgtcctcaag 780

ctgctcttgt gttaatggtt tctttttttgt gctcatacgt taaatctatc accgcaaggg 840

ataaatatct aacaccgcgc gtgttgacta ttttacctct ggcggtgata atggttgcat 900

gtactaagta ggttgtatgg aacaacgcat aaccctgaaa gattatgcaa tgcgctttgg 960

gcaaaccaag acagctaaag atcctctaga gcgcccggaa gagagtcaat tcagggtggt 1020

gaat gtg aaa cca gta acg tta tac gat gtc gca gag tat gcc ggt gtc  1069
     Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu Tyr Ala Gly Val
       1               5                  10                  15

tct tat cag acc gtt tcc cgc gtg gtg aac cag gcc agc cac gtt tct  1117
Ser Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala Ser His Val Ser
                  20                  25                  30

gcg aaa acg cgg gaa aaa gtg gaa gcg gcg atg gcg gag ctg aat tac  1165
Ala Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu Asn Tyr
             35                  40                  45

att ccc aac cgc gtg gca caa caa ctg gcg ggc aaa cag tcg ttg ctg  1213
Ile Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser Leu Leu
         50                  55                  60

att ggc gtt gcc acc tcc agt ctg gcc ctg cac gcg ccg tcg caa att  1261
Ile Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser Gln Ile
     65                  70                  75

gtc gcg gcg att aaa tct cgc gcc gat caa ctg ggt gcc agc gtg gtg  1309
Val Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser Val Val
 80                  85                  90                  95

gtg tcg atg gta gaa cga agc ggc gtc gaa gcc tgt aaa gcg gcg gtg  1357
Val Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala Ala Val
                100                 105                 110
```

a' cont.

```
cac aat ctt ctc gcg caa cgc gtc agt ggg ctg atc att aac tat ccg   1405
His Asn Leu Leu Ala Gln Arg Val Ser Gly Leu Ile Ile Asn Tyr Pro
            115                 120                 125

ctg gat gac cag gat gcc att gct gtg gaa gct gcc tgc act aat gtt   1453
Leu Asp Asp Gln Asp Ala Ile Ala Val Glu Ala Ala Cys Thr Asn Val
        130                 135                 140

ccg gcg tta ttt ctt gat gtc tct gac cag aca ccc atc aac agt att   1501
Pro Ala Leu Phe Leu Asp Val Ser Asp Gln Thr Pro Ile Asn Ser Ile
    145                 150                 155

att ttc tcc cat gaa gac ggt acg cga ctg ggc gtg gag cat ctg gtc   1549
Ile Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val
160                 165                 170                 175

gca ttg ggt cac cag caa atc gcg ctg tta gcg ggc cca tta agt tct   1597
Ala Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser
                180                 185                 190

gtc tcg gcg cgt ctg cgt ctg gct ggc tgg cat aaa tat ctc act cgc   1645
Val Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg
            195                 200                 205

aat caa att cag ccg ata gcg gaa cgg gaa ggc gac tgg agt gcc atg   1693
Asn Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met
        210                 215                 220

tcc ggt ttt caa caa acc atg caa atg ctg aat gag ggc atc gtt ccc   1741
Ser Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro
    225                 230                 235

act gcg atg ctg gtt gcc aac gat cag atg gcg ctg ggc gca atg cgc   1789
Thr Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg
240                 245                 250                 255

gcc att acc gag tcc ggg ctg cgc gtt ggt gcg gat atc tcg gta gtg   1837
Ala Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val
                260                 265                 270

gga tac gac gat acc gaa gac agc tca tgt tat atc ccg ccg tca acc   1885
Gly Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Ser Thr
            275                 280                 285

acc atc aaa cag gat ttt cgc ctg ctg ggg caa acc agc gtg gac cgc   1933
Thr Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg
        290                 295                 300

ttg ctg caa ctc tct cag ggc cag gcg gtg aag ggc aat cag ctg ttg   1981
Leu Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu
    305                 310                 315

ccc gtc tca ctg gtg aaa aga aaa acc acc ctg gcg ccc aat acg caa   2029
Pro Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln
320                 325                 330                 335

acc gcc tct ccc cgc gcg ttg gcc gat tca tta atg cag ctg gca cga   2077
Thr Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg
                340                 345                 350
```

a' cont.

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cag gtt tcc cga ctg gaa agc ggg cag tgagcgcaac gcaattaatg          2124
Gln Val Ser Arg Leu Glu Ser Gly Gln
            355                 360

tgagttagct cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt 2184

tgtgtggaat tgtgagcgga taacaatttc acacaggaaa cagctctgca ggcatgcaag 2244

cttatcgaat tctcattcag gcttctgccg ttttggattt aaccgaagat gatttcgatt 2304

ttctgacgag taacaaagtt tggattgcta ctgaccgctc tcgtgctcgt cgctgcgttg 2364

aggcttgcgt tt atg gta cgc tgg act ttg tgg gat acc ctc gct ttc ctg 2415
             Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu
                         365                 370

ctc ctg ttg agt tta ttg ctg ccg tca ttg ctt att atg ttc atc ccg   2463
Leu Leu Leu Ser Leu Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro
    375                 380                 385

tca aca ttc aaa cgg cct gtc tca tca tgg aag gcg ctg aat tta cgg   2511
Ser Thr Phe Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg
390                 395                 400                 405

aaa aca tta tta atg gcg tcg agc gtc cgg tta aag ccg ctg aat tgt   2559
Lys Thr Leu Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys
                410                 415                 420

tcg cgt tta cct tgc gtg tac gcg cag gaa aca ctg acg ttc tta ctg   2607
Ser Arg Leu Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu
            425                 430                 435

acg cag aag aaa acg tgc gtc aaa aat tac gtg cag aag gag           2649
Thr Gln Lys Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
        440                 445                 450

tgatgtaatg tctaaaggta aaaaacgttc tggcgctcgc cctggtcgtc cgcagccgtt 2709

gcgaggtact aaaggcaagc gtaaaggcgc tcgtctttgg tatgtaggtg gtcaacaatt 2769

ttaattgcag gggcttcggc ccttacttga ggataaatta tgtctaatat tcaaactggc 2829

gccga                                                             2834
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a' cont.

<210> 8
<211> 237
<212> PRT
<213> pCSJ Fragment

<400> 8

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Met Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala
  1               5                  10                  15

Arg Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu
            20                  25                  30

Ser Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val
        35                  40                  45
```

```
Gly Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala
     50                  55                  60

Leu Leu Thr Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser
 65                  70                  75                  80

Ile Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Gln Pro
                 85                  90                  95

Ser Leu Arg Ser Glu Tyr Glu Tyr Pro Val Phe Ser His Val Gln Ala
            100                 105                 110

Gly Met Phe Ser Pro Lys Leu Arg Thr Phe Thr Lys Gly Asp Ala Glu
        115                 120                 125

Arg Trp Val Ser Thr Thr Lys Lys Ala Ser Asp Ser Ala Phe Trp Leu
    130                 135                 140

Glu Val Glu Gly Asn Ser Met Thr Ala Pro Thr Gly Ser Lys Pro Ser
145                 150                 155                 160

Phe Pro Asp Gly Met Leu Ile Leu Val Asp Pro Glu Gln Ala Val Glu
                165                 170                 175

Pro Gly Asp Phe Cys Ile Ala Arg Leu Gly Gly Asp Glu Phe Thr Phe
            180                 185                 190

Lys Lys Leu Ile Arg Asp Ser Gly Gln Val Phe Leu Gln Pro Leu Asn
        195                 200                 205

Pro Gln Tyr Pro Met Ile Pro Cys Asn Glu Ser Cys Ser Val Val Gly
    210                 215                 220

Lys Val Ile Ala Ser Gln Trp Pro Glu Glu Thr Phe Gly
225                 230                 235
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a' cont.

<210> 9
<211> 360
<212> PRT
<213> pCSJ Fragment

<400> 9

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Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu Tyr Ala Gly Val Ser
  1                 5                  10                  15

Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala Ser His Val Ser Ala
             20                  25                  30

Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu Asn Tyr Ile
         35                  40                  45

Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser Leu Leu Ile
     50                  55                  60

Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser Gln Ile Val
 65                  70                  75                  80

Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser Val Val Val
```

```
                    85                  90                  95

Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala Ala Val His
            100                 105                 110

Asn Leu Leu Ala Gln Arg Val Ser Gly Leu Ile Ile Asn Tyr Pro Leu
        115                 120                 125

Asp Asp Gln Asp Ala Ile Ala Val Glu Ala Ala Cys Thr Asn Val Pro
    130                 135                 140

Ala Leu Phe Leu Asp Val Ser Asp Gln Thr Pro Ile Asn Ser Ile Ile
145                 150                 155                 160

Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val Ala
                165                 170                 175

Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser Val
            180                 185                 190

Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg Asn
        195                 200                 205

Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met Ser
    210                 215                 220

Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro Thr
225                 230                 235                 240

Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg Ala
                245                 250                 255

Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val Gly
            260                 265                 270

Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Ser Thr Thr
        275                 280                 285

Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg Leu
    290                 295                 300

Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu Pro
305                 310                 315                 320

Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln Thr
                325                 330                 335

Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg Gln
            340                 345                 350

Val Ser Arg Leu Glu Ser Gly Gln
        355                 360
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a' cont.

<210> 10
<211> 91
<212> PRT
<213> pCSJ Fragment

<400> 10
Met Val Arg Trp Thr Leu Trp Asp Thr Leu Ala Phe Leu Leu Leu Leu
1 5 10 15

Ser Leu Leu Leu Pro Ser Leu Leu Ile Met Phe Ile Pro Ser Thr Phe
20 25 30

Lys Arg Pro Val Ser Ser Trp Lys Ala Leu Asn Leu Arg Lys Thr Leu
35 40 45

Leu Met Ala Ser Ser Val Arg Leu Lys Pro Leu Asn Cys Ser Arg Leu
50 55 60

Pro Cys Val Tyr Ala Gln Glu Thr Leu Thr Phe Leu Leu Thr Gln Lys
65 70 75 80

Lys Thr Cys Val Lys Asn Tyr Val Gln Lys Glu
85 90

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

a' cont

<220>
<223> Description of Artificial Sequence: synthetic primer

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gtaaaatagt caacacgcgc ggtgttagat atttatc 37